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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Perfect score:
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  1835
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1693.5
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2: /SIDS6/gcgdata/geneseq/geneseqp/AA1981.DAT:*

3: /SIDS6/gcgdata/geneseq/geneseqp/AA1982.DAT:*

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length: 2000000000
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  74.0
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Gapop 10.0 , Gapext 0.5
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R40384
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Compugen Ltd
                                                          Sequence encoded b
Chimeric antibody
T84.12 Heavy chain
MAb 55.1 heavy cha
MAb 55.1 heavy cha
Anti-Fas MAb HFE7A
                                                                                                                                                                                                                                                   Description
Mouse anti-Fas ant
Murine anti-Fas an
Antibody F19 chime
                                                                                                                                                                                    Monoclonal antibod Monoclonal antibod
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| _                  |                    | -      |                    |                   | _                  | _                  |                   | -                  |                    | -                  |                    | -                  |        | •                 | _                  | _        |                    |        |                    | -      |                    | -      |        | •        | _       | _      |        |                    |          | -         |                    |        |                    |
|--------------------|--------------------|--------|--------------------|-------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|-------------------|--------------------|----------|--------------------|--------|--------------------|--------|--------------------|--------|--------|----------|---------|--------|--------|--------------------|----------|-----------|--------------------|--------|--------------------|
| 1427               | 1427               | 1427   | 1427.5             | 1429.5            | 1431.5             | 1433               | 1434              | 1439.5             | 1446               | 1446               | 1447               | 1451.5             | 1451.5 | 1455.5            | 1455.5             | 1455.5   | 1456.5             | 1457.5 | 1457.5             | 1457.5 | 1458.5             | 1458.5 | 1458.5 | 1458.5   | 1459.5  | 1461.5 | 1466.5 | 1466.5             | 1489.5   | 1493.5    | 1548               | 1550   | 1550.5             |
| 57.4               | 57.4               | 57.4   | 7.                 | 7.5               | 7.6                | 7                  | 7.                | 7.                 | 8                  | 8                  | 8                  | 8                  | 8      | 8                 | œ<br>•             | 8        | 58.6               | 8      | 8                  | 8      | 8                  | ۳.     | Θ.     | .8       | œ       | 8      | 9      | 9                  | 9        | 0         | ۲.                 | ۲.     | 2                  |
| 452                | 452                | 452    | 476                | 468               |                    | 448                | 448               | 470                | 463                | 463                | 467                | 595                | 481    | 468               | 464                | 464      | 652                | 470    | 470                | 470    | 470                | 470    | 470    | 470      | 470     | 470    | 449    | 449                | 472      | 470       | 454                | 465    | 472                |
| . 21               | 21                 | 20     | 14                 | 20                | 20                 | 17                 | 14                | 21                 | 18                 | 18                 | 22                 | 20                 | 13     | 13                | 18                 | 18       | 19                 | 21     | 21                 | 19     | 21                 | 21     | 21     | 19       | 21      | 21     | 19     | 14                 | 20       | 21        | 14                 | 16     | 20                 |
| Y77766             | 3032               | Y29458 | R31023             | W85689            | W85692             | R97376             | R43673            | W90936             | W14940             | W14939             | в36210             | W86003             | R24442 | R28808            | W14938             | W14941   | W48650             | W90926 | B14776             | W83036 | W90935             | W90929 | в14779 | W83037   | W90934  | W90933 | W49816 | R43339             | Y50166   | в08026    | R30774             | R66758 | 0                  |
| Humanised anti-IL- | Humanised anti-IL- | immur. | Antibody D heavy c | D9D10 heavy chain | MoTAbII fusion pro | Murine anti-BGH MA | Mouse anti-bovine | Humanised HFE7A de | 3F4 (Chimeric) hum | 3F4 (Chimeric) hum | Human immune syste | Anti-5T4 single ch | æ      | pre-5A8 humanised | Murine anti-porcin | man IgG4 | Heavy chain of hmA | HFE7   | Humanised anti-Fas | humani | Humanised anti-Fas | HFE7A  | a      | humanise | anti-Fa | ω      |        | Completely humanis | haped F1 | c anti-CD | H52H4-160 murine a | a      | Chimeric mouse/hum |

## ALIGNMENTS

OK3T; light chain; humanised antibodies; CDR-grafting.

Monoclonal antibody OK3T heavy chain.

03-OCT-1991 (first entry)

R13061;

R13061 standard; Protein;

468 AA

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WPI; 1991-222915/30
                                                                                                             Key
           Adair JR,
                                 21-DEC-1990;
21-DEC-1989;
                                                                                            Protein
                      (CELL-) CELLTECH LTD
                                                   21-DEC-1990;
                                                              11-JUL-1991.
                                                                          WO9109967-A.
                                                                                                      Peptide
                                                                                                                        Mus musculus.
           Athwal DS,
                                 90WO-GB02017.
89GB-0028874.
                                                   90WO-GB02017
                                                                                      /label= light chain
                                                                                                /label= signal peptide
                                                                                                           Location/Qualifiers
           Emtage JS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
 Region
                    Region
                                          Peptide
                                                                         cytotoxic
                                                                                  anti-snake small neurotoxin antibody; heavy chain; IgG2;
immunoglobulin; bispecific bivalent antibody; cell-targetting;
                                                                                                                 Monoclonal antibody M(alpha)2-3 Heavy-chain
                                                                                                                                                                               R40384 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDR-grafting experiments to prepare humanised antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The OK3T heavy chain sequence was deduced from the cDNA sequence isolated from a library prepared from OK3T producing cells. The library was screened with a probe complementary to a region in the mouse IgG2a constant domain region. The OK3T sequence was used in.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 2b; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; Q12637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New humanised antibodies comprising CDR grafted antibody - with heavy and light chains, for use in in vivo therapy and diagnosis
                                                                                                                                                                                                                                                       420
                                                                                                                                                                                                                                   434
                                                                                                                                                                                                                                                                            374
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                                                                                                                                                                                                                                 ekknwvernsyscsvvheglhnhhttksfsrtpgk 468
                                                                                                                                                                                                                                            KTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCARRAGAYY-FDYWGQGTTLTVSSA 119
                                                                                                                                                                                                                                                                      ppeeemtkkqvtltcmvtdfmpedlyvewtnngktelnykntepvldsdgsyfmysklrv 433
                                                                                                                                                                                                                                                                                     PPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLNM 419
                                                                                                                                                                                                                                                                                                                 redynstlrvvs alpiqhqdwmsgkefkckvnnkdlpapiertiskpkgsvrapqvyvlp\\
                                                                                                                                                                                                                                                                                                                             REDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYILP 359
                                                                                                                                                                                                                                                                                                                                                                      NLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTH 299
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                                                                                                                                                                                                                                                                                                                                                                                                                       YTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKECHKCPAP 239
                                                                                                                                                                                                                                                                                                                                                                                                                                            kttapsvyplapvcgdttgssvtlgclvkgyfpepvtltwnsgslssgvhtfpavlqsdl 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQSGL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ngkfkdkatlttdkssstaymqlssltsedsavyycaryyddhycldywgqgttltvssa 139
                                                                         agent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                      (first entry)
                     20..139
                                                    Location/Qualifiers
          /label= variable
                             /label= signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74.0%;
76.3%;
                                                                                                                                                                               469
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Pred. No. 3.2
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es 60; Indels
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proteins containing two different Ab-derived units (i.e. to publishedific antibodies). When a toxic protein is used in place phoA, the hybrid molecules can be used as cell-targetting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A fragment of the heavy chain (VH + CH1) from the anti-snake small neurotoxin monoclonal antibody M(alpha)2-3 was PCR-amplified from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1993-260351/33
N-PSDB; Q48037.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Fig 3A; 37pp; French.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New immunoglobulin hybrid proteins - with immunoglobulin fragments linked to dimeric protein, for diagnostic or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boulain J, Ducancel
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239
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                                                                                                                                                                             AKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQSG 178
                                                                                                                                                                                                                                                           nenfkgkatltvdtssstaymqlssltsedtavyfcaramgatatlldywgqgttltvss
                                                                                                                                                                                                                                                                                SPKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCARRAG--AYYFDYWGOGTTLTVSS 118
                                                                                                                                                                                                                                                                                                                                                              qiqlqqsgpelvkpgasvkisckasgytftdyyinwvkqkpgqglkwigwiypasgntky 79
  PNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQT
                                                  lytlsssvtvtsstwpsqsitcnvahpasstkvdkkieprgp--tikpcppc----kcpa
                                                                                                                                                     akttapsvyplapvcgdttgssvtlgclvkgyfpepvtltwnsgslssgvhtfpavlqsd
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COMMISSARIAT ENERGIE ATOMIQUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       469 AA;
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/label= c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= joining
253..362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= constant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73.8%; Score 1835; DB 14; 75.7%; Pred. No. 6.2e-111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gillet D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Menez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to produce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8;
                                                                                                                                                           199
        298
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RESULT
P83200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
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       Modified antibodies (Abs) having an altered Fc region with altered binding affinity for an Fc receptor esp. Fc-gamma-R1 may have the following residues replaced: 234, 235, 236 and 237; 235 by Glu, and at least one of the others by Ala. Those with altered binding affinity for Clq may have an altered CH2 domain in which one of the
                                                                                                                           N-PSDB;
                                                                                                                                     WPI; 1988-285543/40
                                                                                                                                                         Winter
                                                                                                                                                                                                                         01-DEC-1987;
18-MAR-1987;
                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                 effector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P83200 standard;
following residues of the heavy chain have been changed
                                                                  Example; Fig 3; 42pp;
                                                                                                                                                                                                                                                                                          W08807089-A
                                                                                                                                                                                                                                                                                                                                          Domain
                                                                                                                                                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                          (MEDI-)
                                                                                                                                                                                                      10-AUG-1987;
18-MAR-1988;
                                                                                                                                                                                                                                                     18-MAR-1988;
                                                                                                                                                                                                                                                                        22-SEP-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                          mmunoglobulin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       419
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vekknwvernsyscsvvheglhnhhttksfsrtpgk 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYIL 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hredynstlrvvsalpiqhqdwmsgkefkckvnnkdlpapiertiskpkgsvrapqvyvl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pnllggpsvfifppkikdvlmislspivtcvvvdvseddpdvqiswfvnnvevhtaqtqt 313
                                                                                                                                                        GP,
                                                                                               'n
                                                                                                                                                                           MEDICAL
                                                                                            IgG class antibody - having at
in the constant portion altered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                 molecule;
                                                                                                                                                       Duncan AR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                      120..234
/label= CH3
235..341
                                                                                                                                                                                                      87GB-0018897.
88WO-GB00211.
                                                                                                                                                                                                                         87GB-0028042.
87GB-0006425.
                                                                                                                                                                                             88GB-0025480
                                                                                                                                                                                                                                                     88WO-GB00211
                                                                                                                                                                                                                                                                                                                                                                                                                                                        class gamma; antibody;
                                                                                                                                                                                                                                                                                                                                                                              /label= CH1
98..119
                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                           /label= hinge
120..234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           by mouse 1gG
                                                                                                                                                                                                                                                                                                              note= "This"
                                                                                                                                                                                                                                                                                                                                'label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                constant
                                                                                                                                                                           COUNCIL
                                                                  English.
                                                                                                                                                                                                                                                                                                                                CH3
                                                                                                                                                        Burton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     341
                                                                                                                                                                                                                                                                                                                                                                                                                                               region; heavy chain;
                                                                                                                                                                                                                                                                                                             residue is Leu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gamma 2b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B
                                                                                                                                                       DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                        immune response;
                                                                                              least one aminoacid to alter an effector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       454
                                                                                                                                                                                                                                                                                                             in
                                                                                                                                                                                                                                                                                                             mutant EL235"
                                                                                                                                                                                                                                                                                                                                                                                                                                               complement.
 to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fc receptor;
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RESULT
P93037
ID P9
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Best Local
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                                                                                                                                                                                                                                                               Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             residue with a different side chain; 318 (changed to Val) 320 and 322 (changed to Gin). Those with altered lytic properties, as compared with unmodified Ab may have an altered CH2 domain where residue 297 of the heavy chain has been changed to Ala.
The sequence encodes the heavy chain of MAb KS1/4, used to construct mouse/human chimeric antibodies. KS1/4 is a murine
                                                             Recombinant DNA cpds.
                                                                                                                                                                                                                      EP338767-A.
                                                                                                                                                                                                                                                                                   Chimeric antibody
                                                                                                                                                                                                                                                                                                                             P93037;
                                                                                                                                                                                                                                                                                                                                                 P93037 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                              Claim
                                                   chimeric
                                                                                  N-PSDB;
                                                                                                                 Beavers
                                                                                                                                   (ELIL)
                                                                                                                                                         21-APR-1988;
                                                                                                                                                                                                  25-APR-1989
                                                                                                                                                                                                                                           KS1/4; chimeric
                                                                                                                                                                                                                                                                                                        14-MAR-1990
                                                                                                                                                                              18-APR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQSG
                                                                                           1989-311203/43
                                                                                                                                                                                                                                                                                                                                                                                                  ysklnmktskwektdsfscnvrheglknyylkktisrspgk
                                                                                                                                                                                                                                                                                                                                                                                                                        YSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AQTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDV-----QISWFVNNVEVHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aqtqthredynstirvvstlpiqhqdwmsgkefkckvnnkdlpspiertiskikglvrap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pnleggpsvfifppnikdvlmisltpkvtcvvvdvseddpdvedppgqiswfvnnvevht
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lytmsssvtvpsstwpsqtvtcsvahpassttvdkklepsgpistinpcppckechkcpa 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        336;
                              6,
                                                                                                                ĽS,
                                                                                                                                    ELI LILLY AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                  N91659
                                                   derived
                              page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                               Bumol TF,
                                                                                                                                                                                                                                                                                                        (first entry)
                              50;
                                                                                                                                                       88US-0184522
                                                                                                                                                                              89EP-0303814.
                                                                                                                                                                                                                                          antibody; heavy chain variable region;
                                                   from
                                                                                                                                                                                                                                                                                                                                               protein; 447
                            89pp;
                                                                                                                                                                                                                                                                                   heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72.0%;
98.5%;
                                                                                                                                     ဗ
                                                  producing monoclonal
                              English
                                                                                                                 Gadski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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Pred. No. 3.8e-108;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                   variable
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                                                                                                                 RΑ,
                                                             antibodies -
                                                   antibody
                                                                                                               Weigel
                                                   KS1/4
                                                                                                                 ВЛ
                                                           monoclonal
                                                                                                                                                                                                                                                                                                                                                                                                    341
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antibody

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RESULT
R47450
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 317;
                                                   (CITY )
(YANG/)
WPI; 1994-007204/01
                    Yang
                     Fischer R,
Yang YH;
                                                                                                                          23-DEC-1993.
                                                                                                                                               WO9325237-A.
                                                                                                                                                                                       region;
                                                                                                                                                                                                 Chimeric;
                                                                                                                                                                                                                       T84.12
                                                                                                                                                                                                                                          24-JUN-1994
                                                                                                                                                                                                                                                               R47450
                                                                                                                                                                                                                                                                                   R47450 standard; Protein; 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 which binds to surface antigens on adenocarcinoma cells and the use human C regions avoids immunological problems during treatment.
                                                                                  15-JUN-1992;
                                                                                                     15-JUN-1993;
                                                                                                                                                                                                                                                                                                                                      413
                                                                                                                                                                                                                                                                                                                                                           420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EVQLQQSGPELVKPGASVMISCRTSAYTFTENTVHWVKQSHGESLEWIGGINPYYGGSIF 60
                                                                                                                                                                                                                                                                                                                                     ekknwvernsyscsvvqeglhnhhttksfsrtpgk 447
                                                                                                                                                                                                                                                                                                                                                 KTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQSGL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         addfkgrfafsletsastaflqiqqpqnmrtmatyfcvrfisk--gdywgqgtsvtvssa
                                                                                                                                                                                                                                                                                                                                                                             redynstlrvvs alpiqhqdwms gkefkckvnnkdlpapiertiskpkgsvrap qvyvlp
                                                                                                                                                                                                                                                                                                                                                                                                                                                              nllggpsvfifppkikdvlmislspivtcvvvdvseddpdvqiswfvnnvevhtaqtqth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ytlsssvtvtsstwpsqsitcnvahpasstkvdkkieprgp--tikpcppc----kcpap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPKFKGKATLTVDKSSSTAYMELRS-LTSEDSAVYYCARRAGAYYFDYWGQGTTLTVSSA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qiqlvqsgpelkkpgetvkisckasgytftnygmnwvkqtpgkglkwmgwintytgepty
                                                                                                                                                                                                                                                                                                                                                                                                  PPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLNM
                                                   CITY
YANG
                                                                                                                                                                                      c; carcinoembryonic antigen; CCA; murine; mouse; constant;
transform; myeloma cell; light chain; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               447 AA;
                               Paxton
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                                                   Y.
                                                                                                                                                                                                                      chain
                                                                                                                                                                                                                                          (first entry)
                                                                                  92US-0904074
                                                                                                      93WO-US05709
                                                              HOPE
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69.7%;
                               Shively
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Pred. No. 8e-
                                                                                                                                                                                                                                                                                   AA
                               JE,
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                              P
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                             Yang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9;
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                                                                                                                                                                                                                                                                                                                                                                               412
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RESULT
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Best Local S
Matches 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequences (Q54651-52) show the light and heavy chain cDNAs of murine 784.12. The 784.12 antibody is directed against the tumour marker carcinoma embryonic antigen, and is useful for tumour imaging and immunotherapy.

The amino acid sequence given in the specification has been incorrectly identified as a nucleic acid sequence, therefore unacceptable characters have been represented as an 'N'.
                                                                                           21-NOV-1995
                                                                                                                                       R76088 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New chimaeric T84.12 antibody active against carcinoembryonic antigen - has murine variable and human constant regions, also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The amino acid sequence given below has been derived from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; Q54652
                                                                                                                                                                                                    440
                                                                                                                                                                                                              417 LNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 454
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                                                                                                                                                                                                                                                                                              320 gthredynstlrvvsalpiqhqdwmsgkefkckvnnkdlpapiertiskpkgsvrapqvy
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                                                                                                                                                                                                                                                                                                                                                                                        QTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVY
                                                                                                                                                                                                                                                                                                                                          vlpppeeemtkkqvtltcmvtdfmpediyvewtnngktelnykntepvldsdgsyfmysk
                                                                                                                                                                                                                                                                     ILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vdsvkgrftvsrdnarnilylqmsslrsedtamyycari--dyyggggfgywgqgtlatv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EVQLQQSGPELVKPGASVMISCRTSAYTFTENTVHWVKQSHGESLEWIGGINPYYGGSIF 60
                                                                                                                                                                                                 lrvekknwvernsyscsvvheglhnyhttksfsrtpgk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCARRAGAYY - - - - FDYWGQGTTLTV 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the indexer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               477 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                           (first entry)
                                                                                                                                       Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67.2%; Score 1670.5; 69.0%; Pred. No. 2.66 tive 54; Mismatches
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es 75;
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Antigen binding structure; complementarity determining region; CA55.1; colorectal cancer; tumor-associated antigen; hybridoma; monoclonal antibody; MAb; immunotherapy; therapy; diagnosis; transgenic animal; transgenic plant; antibody engineering;

immunotoxin

55.1

chain.

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Best Local S
Matches 304
                                                                                                                                                                                                                                                                                                                                                                     MAb 55.1 (ECACC 93081901) recognises the colorectal tumor-associated antigen CA55.1. cDNAs for the heavy (Q94037) and light (Q94036) chains of 55.1 were isolated, and F(ab)', F(ab)2, Fab, Fv, scFv or V-min humanized 55.1 constructs have been expressed in myeloma cells and E. coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antigen binding structures containing CDRs recognising the antigen - produced by hybridomas and host cells, for use ir diagnosis and therapy of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig.15; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-JUN-1994;
03-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1995-215262/28
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          LPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKL
                                                                              THREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYI
                                                                                                                                                                  SAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQS 177
                                                                                                                                                                                                          nekfknkatltvdkssttaymqlssltsedsavyy careraygyddamdywgqgtsvtvs\\
                                                                                                                                                                                                                      SPKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCAR-RAGAY--YFDYWGQGTTLTVS 117
                                                                                                                                                                                                                                                              EVQLQQSGPELVKPGASVMISCRTSAYTFTENTVHWVKQSHGESLEWIGGINPYYGGSIF 60
ippp keqmakdkvsltcmitdffpeditvewqwngqpaenykntqpimdtdgsyfvyskl\\
                                        preeqfnstfrsvselpimhqdwlngkefkcrvnsaafpapiektisktkgrpkapqvyt\\
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                                                                                                                                                                                                                                                                                                 Conservative
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93GB-0024819
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20..464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Mat_protein
/note= "claim 3, page
                                                                                                                                                                                                                                                                                                         64.1%;
66.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sig_peptide
                                                                                                                                                                                                                                                                                                55;
                                                                                                                                                                                                                                                                                             Score 1594.5;
Pred. No. 2e-9:
55; Mismatches
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                                                                                                                                                                                                                                                                                                         2e-95;
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Best Local Similarity
                                                                                                                                                                                                                                   An antigen binding structure is based on the CDRs (given in R76078-84) of the heavy (R76085) and light (R76086) chains of MAb 55.1 (ECACC 93081901), which recognises the colorectal tumor-associated antigen CAS5.1. It is optionally humanized and in the form F(ab')2, F(ab), Fab, Fv, scFv or V-min, and is produced in transgenic animals or plants.
                                                                                                                                                                                                                                                                                                                  Claim 3; Page 97-98; 121pp; English.
                                                                                                                                                                                                                                                                                                                                       Antigen binding structures containing antigen - produced by hybridomas and I diagnosis and therapy of cancer
                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1995-215262/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-JUN-1994;
03-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CA55.1; colorectal cancer; tumor-associated antigen; hybridoma; monoclonal antibody; MAb; immunotherapy; therapy; diagnosis; transgenic animal; transgenic plant; antibody engineering; humanized antibody; immunotoxin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAb
                                                                                                                                                                                                                Sequence
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 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55.1 heavy chain.
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GLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKECHKCP
                                                                           SPKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCAR-RAGAY--YFDYWGQGTTLTVS 117
                                                                                                                                  EVQLQQSGPELVKPGASVMISCRTSAYTFTENTVHWVKQSHGESLEWIGGINPYYGGSIF 60
                                                                                                                                                                                                                                                                                                                                                                                                             MS,
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                     nekfknkatltvdkssttaymqlssltsedsavyycareraygyddamdywgqgtsvtvs
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                                            SAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQS 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           binding structure;
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93GB-0024819
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                                                                                                                                                         54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complementarity determining
                                                                                                                                                        Score 1590.5; DB 16;
Pred. No. 3.5e-95;
54; Mismatches 84;
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RESULT
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 08-OCT-1997;
01-APR-1997;
25-JUN-1997;
                                    30-MAR-1998;
                                                                     AU9859701-A
                                                                                                                                                                                                                                   Key
                                                                                                                                                                                                                                                                                 myasthenia gravis; multiple sclerosis; Basedow's disease;
thrombopenia purpura; insulin-dependent diabetes; allergy;
atopy; arteriosclerosis; myocarditis; cardiomyopathy;
glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                               W83041 standard;
                                                                                                      Region
                                                                                                                              Region
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                                                                                                                                                                       Region
                                                                                                                                                                                        Region
                                                                                                                                                                                                         Protein
                                                                                                                                                                                                                                                  Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                               15-MAR-1999
                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                    apoptosis; HFE7A; autoimmune disease; Hashimoto's diseas systemic lupus erythematosus; graft versus host disease; Sjogren syndrome; pernicious anaemia; Addison's disease;
                                                                                                                                                                                                                                                                                                                                                     HFE7A; monoclonal antibody; mouse; Fas; humanised antibody; anomotosis: HFE7A; autoimmune disease; Hashimoto's disease;
                                                                                                                                                                                                                                                                                                                                                                             Anti-Fas MAb HFE7A heavy chain.
                                                                                                                                                                                                                                                                                                                           scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
                                                                                                                                                                                                                                                                                                                    rheumatoid arthritis; autoimmune haemolytic anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENVKDTAPVLDSDGSYFIYSKL
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 97JP-0276064.
97JP-0082953.
97JP-0169088.
                                    98AU-0059701
                                                                                                    /label= CDR_H2
/note= "claim 9"
118..128
                                                                                                                                                                                                        /label=
20..464
                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                        /label= Mat_protein 20..140
                                                                                    /label= CDR_H3
/note= "claim 9"
                                                                                                                                                                         141..464
                                                                                                                                     /note= "claim 9"
                                                                                                                                                /label= CDR_H1
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                                                                                                                                                                                                                                                                                                                                                                                                                               Protein; 464
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                                                                                                                                                                                                                                                                         therapy; complementarity determing region;
                                                                                                                                                               Constant
                                                                                                                                                                                                                Sig_peptide
                                                                                                                                                                                                                                                                                   AIDS;
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Best Local Similarity
Matches 298; Conserv
                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diseases e.g.
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Hideyuki H,
O, Nobufusa
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CC Chain was obtained from HFETA-secreting hybridoma (FERN BP-5828) CC RNA by RT-PCR (see V70125-26). The invention provides humanised CC HFETA antibodies (see W83031-37) produced by CDR grafting. These CC antibodies are capable of inhibiting Fas-induced apoptosis in normal cells cells. They are used to evaluate, in animal models, treatments of CC cells. They are used to evaluate, in animal models, treatments of CC ciseases that involve Fas/Fas ligand interactions, and also to treat such diseases, including autoimmune disease (e.g. systemic lupus crythematosus, Hashimoto's disease, graft versus host disease, CC sjogren syndrome, pernicious anaemia, Addison's disease, rheumatoid arthritis, autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura and insulin-dependent diabetes), allergies, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reference Example 4; Page 187-188; 292pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             myocarditis, hepatitis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antibodies and proteins bind used to evaluate drugs in animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                is the amino acid of the heavy chain of murine anti-human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibody HFE7A
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(, Tohru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            conserved epitope of Fas antigen - models and to treat Fas-associated allergy, atopy, arteriosclerosis,
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LPPPABQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKL 417 GLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKECHKCP EVQLQQSGPELVKPGASVMISCRTSAYTFTENTVHWVKQSHGESLEWIGGINPYYGGSIF preeqfnstfrsvselpimhqnwlngkefkcrvnsaafpapiektisktkgrpkapqvyt THREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYI 357 dlytlsssvtvpsstwpsqtvtcnvahpasstkvdkkivp----rdc-gckpc-ict SAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQS SPKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCARR---AGAYYFDYWGQGTTLTVS 117 ipppkeqmakdkvsltcmitdffpeditvewqwngqpaenykntqpimntngsyfvyskl Conservative 62.9%; =: :: = = : = : 58; Score 1564.5; DB 19; Length 464; Pred. No. 1.7e-93; B; Mismatches 86; Indels 15; Gaps 177 79 60 307 297 250 237

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                                                                                                                                                                                                                                                                     The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFE7A, or a humanised version of HFE7A containing identical CDRs (complementarity determining regions) to antibody HFE7A. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, arteriosclerosis, myocarditis, cardiomyopathy, arteriosclerosis, myocarditis, cardiomyopathy, allergy, aplastic anaemia (panmyalophthisis), hepatitis, AIDS and organ graft rejection. The present sequence represents the heavy chain of the murine anti-human Fas monoclonal antibody HFE7A, which is produced by hybridoma HFE7A (FERM-BP-5828).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains anti-Fas antibody -
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                                                                                                                                                                                                                                                Sequence
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                                                                                                                              EVQLQQSGPELVKPGASVMISCRTSAYIFTENTVHWVKQSHGESLEWIGGINPYYGGSIF
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                                                                                                                                                                                       Similarity
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65.2%;
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                                                                                                                                                                           58;
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Pred. No. 1.7e-93;
8; Mismatches 86; 1
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panmyelophthisis;
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molecule

Example

reference

4; Page 100-102;

263pp; English.

apoptosis

selectively

This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas, ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding bet Fas and its ligand. The products of the invention have anti-inflamed as the system of the invention have anti-inflamed fas and its ligand.

inhibiting binding between ention have anti-inflammatory,

Fas/Fas

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fas; antibody; murine; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
                                                                                                           New humanized anti-Fas antibody, useful for treating inflammatory or autoimmune disease, induces apoptosicells with abnormal Fas-Fas ligand systems
                                                                                                                                                                  N-PSDB;
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30-SEP-1998;
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in
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CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
CC apoptosis by binding to cell surface Fas or inhibit it by competitive
CC inhibition of ligand binding. (I) are used to treat and/or prevent
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
CC inhibit apoptosis in normal cells but selectively induce it in abnormal
CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
CC cells. They bind to both human and murine Fas, so can be evaluated in
CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
CC inducing a human anti-murine antibody response. This sequence represents
CC method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
              chimeric mouse/human heavy chain variable region (chf19HC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1564.5; DB Pred. No. 1.7e-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                 464
                                                                                                                                                                                                                                                  454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 21; Length 464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               139
                                                                                                                                                                                                                                                                                                                                                         367
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                                                                                                                                                                                                                                                   CC chimeric mouse/human F19 antibody (chF19HC). F19 (AFCC CC Accession number HB 8269) is a murine monoclonal antibody cagainst fibroblast activation protein alpha (FAP). FAP is a cell CC against fibroblast activation protein alpha (FAP). FAP is a cell CC surface molecule of reactive stromal fibroblasts, and its induction CC is a highly consistent molecular trait of the reactive stroma of many CC types of epithelial cancer. Although F19 may be useful in vitro, e.g., CC for diagnosis, its applications for in vivo use in humans are problematic as it elicits a human anti-mouse response which reduces the efficacy of CC the antibody in patients and impairs continued administration. This CC chimeric antibody was humanised by joining entire murine variable regions CC to human constant regions. However, humanised antibodies produced by this method can still elicit an anti-mouse response in humans, whereas CC method can still elicit an anti-mouse response in humans, whereas CC method can still elicit an anti-mouse response in humans, whereas CC useful for treating cancers e.g., colorectal cancers, non-small cell lung cancers, bladder cancers, band nack cancers, ovarian cancers. CC They are also useful for the detection of activated stromal fibroblasts in a healing wound, inflamed skin or a tumour in a human patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 297; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             variable region; producibility; treatment; cancer; colorectal; lung; breast; head; neck; ovarian; lung; bladder; pancreatic; metastasis; detection; wound healing; skin inflammmation; tumour; immunogenicit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric - Mus:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    humanisation; complementarity determining region; CDI reactive stroma; fibroblast; epithelial cancer; diagrimmune response; framework sequence; constant region;
                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Fig 18; 143pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antibody protein, useful for treating cancer and presence of activated stromal fibroblasts in healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-621833/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Park JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chimeric; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibody; monoclonal; F19; fibrinogen activation protein alpha; FAP; humanisation; complementarity determining region; CDR; CDR grafting;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP953639-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
 61
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 qkfkgratltvgkssstayme
                                       PKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCARRAGAYYF-----DYWGQGTTLT 115
                                                                        VQLQQSGPELVKPGASVMISCRTSAYTFTENTVHWVKQSHGESLEWIGGINPYYGGSIFS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Garin-Chesa P,
                                                                                                                                                                                                                                                 453 AA;
                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98EP-0107925
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sapiens
62.7%; Score 1559; DB 20; 64.6%; Pred. No. 3.8e-93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bamberger U,
                                                                                                                                                     61;
                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leger 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnosis;
                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saldanha J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for imaging wound or inflamed
                                                                                                                                                                                              453;
                                                                                                                                                        14;
                                                                                                                                                        Gaps
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116 VSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALL 175

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Y50157
 Park JE,
                                          30-APR-1998;
                                                                                   03-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric mouse/human F19 antibody heavy chain.
                    (BOEH ) BOEHRINGER INGELHEIM INT GMBH
                                                              30-APR-1998;
                                                                                                     EP953639-A1
                                                                                                                                                                                                                                                                                                                           Chimeric
                                                                                                                                                                                                                                                                                                                                                                                         variable
                                                                                                                                                                                                                                                                                                                                                                                                           reactive stroma;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Y50157 standard;
                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                                                                                     detection;
                                                                                                                                                                                                                                                                                                                                                                            immune response; framework sequence; constant region;
variable region; producibility; treatment; cancer; colorectal;
breast; head; neck; ovarian; lung; bladder; pancreatic; metast;
                                                                                                                                                                                                                                                                                                                                                                                                                       humanisation;
                                                                                                                                                                                                                                                                       Protein
                                                                                                                                                                                                                                                                                            Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vytlppsreemtknqvsltclvkgfypsdiavewesngqpennykttppvldsdgsffly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VYILPPPAEQLSRKDVSLTCLVVGENPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q-SGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKECH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -cpapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnwyvdgvevhna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qssglyslssvvtvpssslgtqtyicnvnhkpsntkvdkkvepkscdkt-htcpp----
                                                                                                                                                                                                                                                                                                                            . .
 Garin-Chesa
                                                                                                                                                                                                                                                                                                                                                         heavy chain.
                                                                                                                                                                                                                                                                                                                                                                   wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                          oclonal; F19; fibrinogen activation protein alpha; complementarity determining region; CDR; CDR grafima; fibroblast; epithelial cancer; diagnosis;
                                                                                                                                                                                                                                                                                                                         sp.
o sapiens.
                                         98EP-0107925
                                                            98EP-0107925
                                                                                                                                                                  /note= "(
143..144
                                                                                                                                                                                                                              /note= "Mature chimeric mouse/human 20..143 /note= "Mature mouse F19 heavy chain 50..54
                                                                                                                                                                                     /note=
118..1
                                                                                                                                                                                                                                                                      /note= "Leader peptide" 20..472
                                                                                                                                    144..472
                                                                                                                                                                                                           69..85
                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                          /note=
                                                                                                                                                       /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein; 472
                                                                                                                                                                                                                    note=
                                                                                                                                                                                        ..132
P,
                                                                                                                                                                                               "CDR
                                                                                                                                            "mRNA splicing between these
                                                                                                                                                                             "CDR 3"
                                                                                                                                                                                                                                      "Mature mouse F19 heavy chain variable region
                                                                                                                         "Human gamma-1 heavy chain constant region"
                                                                                                                                                                                                                   "Complementarity determining
Bamberger U,
                                                                                                                                                                                                                                                                                                                                                                    skin
                                                                                                                                                                                                                                                                                                                                                                   inflammmation;
                                                                                                                                                                                                                                                                                                                                                                           bladder; pancreatic;
                                                                                                                                            residues"
Leger 0,
                                                                                                                                                                                                                                                                                                                                                                   tumour;
                                                                                                                                                       Ala
Saldanha
                                                                                                                                                       6
                                                                                                                                                                                                                   region (CDR) 1"
                                                                                                                                                                                                                                                           F19 heavy chain"
                                                                                                                                                       be
                                                                                                                                                                                                                                                                                                                                                                             rectal; lung;
metastasis;
                                                                                                                                                       inserted
                                                                                                                                                                                                                                                                                                                                                                                                                    grafting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           413
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        is a highly consistent molecular trait of the reactive stroma of many types of epithelial cancer. Although F19 may be useful in vitro, e.g., for diagnosis, its applications for in vivo use in humans are problematic as it elicits a human anti-mouse response which reduces the efficacy of the antibody in patients and impairs continued administration. This chimeric antibody was humanised by joining entire murine variable regions to human constant regions. However, humanised antibodies produced by this method can still elicit an anti-mouse response in humans, whereas antibodies humanised via CDR (complementarity determining region) grafting are less immunogenic in humans. Humanised T19 antibodies are useful for concernal contracts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful for treating cancers e.g., colorectal cancers, non-small cell lung cancers, breast cancers, head and neck cancers, ovarian cancers lung cancers, bladder cancers, pancreatic cancers and metastatic cancers They are also useful for the detection of activated stromal fibroblasts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents the heavy chain of a chimeric mouse/human Fantibody. F19 (ATCC Accession number HB 8269) is a murine monoclonal antibody against fibroblast activation protein alpha (FAF). FAF is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antibody protein, presence of activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            surface molecule of reactive stromal fibroblasts, and its induction
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432
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                                   YSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK
                                                                                         QVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFI 413
                                                                                                                                           aktkpreegynstyrvvsvltvlhqdwlngkeykckvsnkalpapiektiskakgqprep
                                                                                                                                                            AQTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAP
                                                                                                                                                                                                                --cpapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnwyvdgvevhn
                                                                                                                                                                                                                                 HKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKYTCVVVDVSEDDPDVQISWFVNNVEVHT
                                                                                                                                                                                                                                                                                                           LQ-SGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKEC
                                                                                                                                                                                                                                                                                                                                                      TVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPAL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                   evqlqqsgpelvkpgasvkmscktsrytfteytihwvrqshgkslewigginpnngipny 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      healing wound,
yskltvdksrwqqgnvfscsvmhealhnhytqkslslspgk
                                                                      qvytlppsreemtknqvsltclvkgfypsdiavewesngqpennykttppvldsdgsffl
                                                                                                                                                                                                                                                                                     lqssglyslssvvtvpssslgtqtyicnvnhkpsntkvdkkvepkscdkt-htcpp----
                                                                                                                                                                                                                                                                                                                                                                                                                                 nqkfkgratltvgkssstaymelrsltsedsavyfcarrriaygydeghamdywgqgtsv
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297; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27; 143pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inflamed skin or a tumour in a human patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful for treating stromal fibroblasts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1550.5; DB 20;
Pred. No. 1.4e-92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer and in healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 20; Length 472;
                                     454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for imaging wound or inflamed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60
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RESULT R66758

R66758 standard; Protein; 465

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Best Local
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                                                                                                                                                                                                                                            monoclonal antibody. The cDNAs were incorporated into a Ti plasmid vector, which was incorporated into A. tumefaciens. The resultant plant expression vector was used to transform tobacco plants, making them TMV resistant, the plants could also be biofarmed for the prodn. of anti-virus antibodies.
                                                                                                                                                                                                                                                                                                                                                               Transformed plant producing animal-derived anti-virus antibody esp. tobacco plants producing anti-tobacco mosaic virus monoclonal antibody
                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                       Q79929 and Q79930 encode R66757 and R66758, the light and heavy chains of an animal derived anti-tobacco mosaic virus (TMV)
                                                                                                                                                                                                                                                                                                                                        Example 2; Pages 14-15; 26pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1995-040220/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-MAY-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anti-tobacco mosaic virus monoclonal Ab heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                              (NISB ) JAPAN TOBACCO INC. (KURS ) KURARAY CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             heavy chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tobacco mosaic virus; TMV; monoclonal antibody;
                        140
 177
                                              117
                                                                     80
                                                                                            61
                                                                                                                  20
                                                                                                                                                                            Local Similarity
                                                                                                                           1 EVQLQQSGPELVKPGASVMISCRTSAYTFTENTVHWVKQSHGESLEWIGGINPYYGGSIF 60
SGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKECHKC
                 SSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQ 176
                                                               SPKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCARRAG----AYYFDYWGQGTTLTV 116
                                                                                                                qvqlqqsgaelarpgasvklsckasgytftsywmqwvkqrpgqglewigaiypgngdtry 79
                                                                                                                                                                                                                          465 AA;
                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            virus-resistant plants; biofarming.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93JP-0131208.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93JP-0131208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label=
20..128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          142..465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "variable heavy domain"
129..141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= leader
20..465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note-
                                                                                                                                                                          62.3%; Score 1550; DB 16; 64.4%; Pred. No. 1.5e-92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 - mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "J heavy 4 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "constant heavy domain"
                                                                                                                                                              58;
                                                                                                                                                                 Mismatches
                                                                                                                                                                 9;
                                                                                                                                                                                     Length 465;
                                                                                                                                                               Indels
                                                                                                                                                               16;
                                                                                                                                                              Gaps
236
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RESULT
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                                                                                                                                                              Query Match
Best Local :
                                                                                                                                                Matches 294;
                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                          antibody H52H4-160.
                                                                                                                                                                                                                                                       The sequence is that of the heavy chain of murine anti-CD18
                                                                                                                                                                                                                                                                                 Disclosure; Fig 6A; 126pp; English.
                                                                                                                                                                                                                                                                                                          Humanisation of antibodies - by molecular modelling of the variable domains and alteration by gene conversion mutagenesis
                                                                                                                                                                                                                                                                                                                                                   WPI; 1993-018139/02
                                                                                                                                                                                                                                                                                                                                                                             Carter PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R30774;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R30774 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                14-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-DEC-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09222653-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Humanisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H52H4-160 murine anti-CD18 antibody heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-MAY-1993
115 TVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPAL 174
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                                     61 nqrfmdkatlavdkststaymelrsltsedsgiyycarwrglnygfdvryfdvwgagttv 120
                                                                                                                                               Local Similarity 63.8 ses 294; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14
                                                    qvqlqqsgpelvkpgasvkiscktsgytfteytmhwmkqshgkslewiggfnpknggssh 60
                                                                                                        EVQLQQSGPELVKPGASVMISCRTSAYTFTENTVHWVKQSHGESLEWIGGINPYYGGSIF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSK 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              \verb|tipppkeqmakdkvs|| \verb|tcmitdff|| peditvewqwngqpaenykntqpimntngsyfvysk||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qpreeqfnstfrsvselpimhqdwlngkefkcrvnsaafpapiektisktkgrpkapqvy
                                                                                                                                                                                                                454 AA;
                                                                                                                                                                                                                                                                                                                                                                           Presta LG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rapid;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           92WO-US05126
                                                                                                                                                          62.2%;
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                                                                                                                                               59;
                                                                                                                                               Score 1548; DB Pred. No. 2e-92; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3
                                                                                                                                                                        DB 14;
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                                                                                                                                                94;
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                                                                                                                                                14;
                                                                                                                                               Gaps
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Example 1; Fig 2A-C; 65pp; English

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                                                                                                                                                                                                                                                                                                                                                                                           complement system; require immunogiobulin; immunoglobulin; IgG; host immune cell; programma receptor; cytotoxic effector cell; host immune cell; programmed cell death; allergic disorder; cancer; autoimmune disease; allergic asthma; atopic dermatitis; Crohn's disea allergic bronchopulmonary aspergillosis; allergic rhinitis; Graves's disease; food allergy; allergic contact dermatitis; cancer; B-cell lymphoma; rheumatoid arthritis; ulcerative colitis; psoriasis; pigeon breeder's disease; hepatitis; leprosy; Lyme disease; diabetes mellitus; candidiasis: aplastic anamounts.
           Genetically engineering immunoglobulin (Ig) G/IgG dimers for the treatment of cancers, allergic disorders and autoimmune conditions
                                                WPI; 2000-514811/46.
N-PSDB; A63531.
                                                                                     Braslawsky GR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A dimeric anti-CD20 heavy chain polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B08026 standard;
                                                                                                              (IDEC-) IDEC
                                                                                                                                                                                                                  WO200044788-A1
                                                                                                                                                                                                                                                                                                                                                          Chimeric
                                                                                                                                                                                                                                                                                                                                                                      Chimeric
                                                                                                                                         28-JAN-1999;
                                                                                                                                                                28-JAN-2000; 2000WO-US01893
                                                                                                                                                                                         03-AUG-2000
                                                                                                                                                                                                                                                                                            Protein
                                                                                                                                                                                                                                                                                                                    Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tvssastkgpsvfplapsskstsggtaalgclvkdyfpepvtvswnsgaltsgvhtfpav
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                                                                                     Hanna
                                                                                                                                                                                                                                                      141..470
                                                                                                                                                                                                                                                                                          /note= "signal peptide" 20..140
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                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                           /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein;
                                                                                                                                                                                                                                         "human gamma 1 heavy chain constant region"
                                                                                                                                                                                                                                                                 "murine anti-human region"
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                                                                                     Hariharan K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B
                                                                                      Labarre
                                                                                                                                                                                                                                                                              CD20 heavy chain
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                                                                                                                                                                                                                                                                               variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                           disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       engineering a monoclonal antibody to introduce a cysteine molecule

which inhibits formation of intramolecular disulphide bridges between

csister heavy chains on the same antibody molecule. The dimer is a

chomodimer or heterodimer that is capable of activating components of the

ccomplement system, and has the ability to activate and kill cells via the

ccomplement cascade. The dimer is also capable of binding to Fogamma

creceptors on cytotoxic effector cells and on host immune cells, and is

ccapable of initiating programmed cell death. The IgG/IgG dimers may be

used to treat allergic disorders, cancers and autoimmune diseases such

as allergic asthma, allergic bronchopulmonary aspergillosis, allergic

crininitis, atopic dermatitis, Crohn's disease, Graves's disease, food

cc llergies, allergic contact dermatitis, CLL cancers and/or B-cell

lymphomas. They may also be used to treat a range of other diseases and

cc disorders such as rheumatoid arthritis, ulcerative colitis, psoriasis,

pigeon breeder's disease, hepatitis, leprosy, Lyme disease, diabetes

mellitus, candidiasis and aplastic anaemia. They are also useful for

induction hyper-cross-libring of membrane antipers and for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mellitus, candidiasis and aplastic anaemia. They are a inducing hyper-cross-linking of membrane antigens and preferential killing of selected cell populations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents a dimeric anti-CD20 light chain polypeptide. The dimeric immunoglobulin is used in the method of invention. The specification describes a method for producing an immunoglobulin (Ig) G/IgG dimer. The method comprises genetically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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Local 5
284;
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                                                                                                        ILPPPAEQLSRKDVSLICLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSK
                                                                                                                                                                                             QTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVY
                                                                                                                                                                                                                                                                                  PAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTAQT
                                                                                                                                                                                                                                                                                                                                            sglyslssvvtvpssslgtqtyicnvnhkpsntkvdkkvepkscdkt-htcpp-----c
                                                                                                                                                                                                                                                                                                                                                                       SGLYTMSSSYTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKECHKC
                                                                                                                                                                                                                                                                                                                                                                                                                                 aastkgpsvfplapsskstsggtaalgclvkdyfpepvtvswnsgaltsgvhtfpavlqs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    {\tt nqkfkgkatltadkssstaymqlssltsedsavyy carstyyggdwyfnvwgagttvtvs}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCARR---AGAYYFDYWGQGTTLTVS: |||||||| |||:||:||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 454
                                                                                                                                                                       kpreegynstyrvvsvltvlhqdwlngkeykckvsnkalpapiektiskakgqprepqvy
                                                                                                                                                                                                                                                            papellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnwyvdgvevhnakt
                                                                                  tlppsrdeltknqvsltclvkgfypsdiavewesngqpennykttppvldsdgsfflysk
ltvdksrwqqgnvfscsvmhealhnhytqkslslcpgk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1493.5; DB Pred. No. 6.7e-89; 2; Mismatches 101
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